FIGURE 1

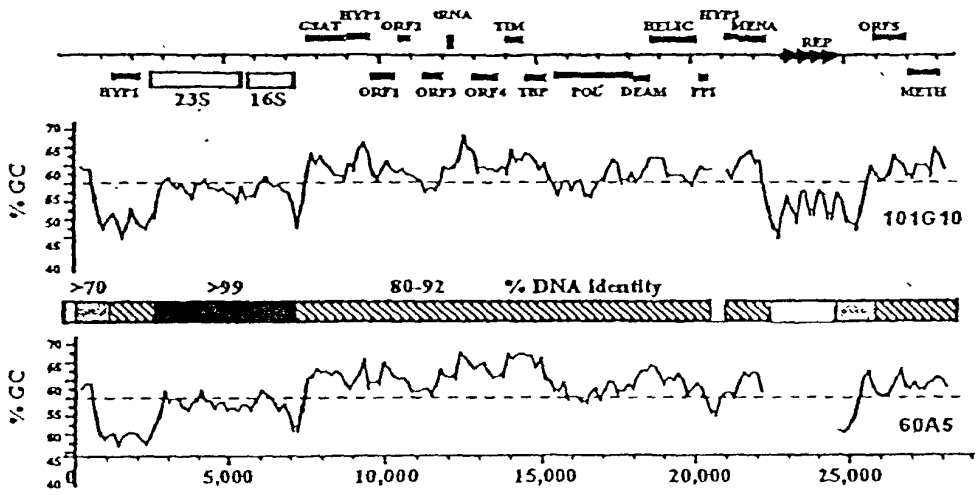

Figure 2

SEQ ID NO.	Gene	Strain	TATA Box	Coding Start	TATA to Start (bp)
81	Hypoth 03	A	AAGCTAGACT TTTAAT TGGG ATCCGGCGGG GCGGCGCATG ---------- ----------		25
82		B	AAGCTAAACT TTTAAT TGGG ATCCGGCGAG CCGGCGCGTG ---------- ----------		
83	Hypoth 02	A	GGAAACTTTG ATTATA CGGG CGTGCTGCCC CGGGGCCCAT G---------- ----------		26
84		B	GGAAACTTTG ATTATA CGGG CGTACATTCC CGGGGCCCAT G---------- ----------		
85	ORF 02	A	AAGGCAAGGT AATAAT AGCC TGCCGTCTGT AACGGCCGTA TG--------- ----------		27
86		B	ACGGCAAGGT AATAAT AGCC TGCCGTCCGT ACCTGCCGTA TG--------- ----------		
87	ORF 03	A	CATGGAACTA GATATT AACC GGTTCCGCGG ATCCCATGCA TG--------- ----------		27
88		B	CATGGAACTA GATAAT AACC GGTCCCGCGG GTACAATGCA TG--------- ----------		
89	PPI	A	ATACCGAGAA GTTATA GCAG GGTATGGAAT GTGCGCGCGC ATG-------- ----------		28
90		B	AGCACGACAA GTTATA GCAG GGTACAAAGG AGCAGCGCAC ATG-------- ----------		
91	GSAT	A	ATCCGCCCTG ATTAAA TTAT GGGGGGAGCG GCCTGCTGCC GTG-------- ----------		28
92		B	ATCCGGCCTC ATTAAA TTAC GGGGGGTACA ACCTGCTGCC GTG-------- ----------		
93	ORF 05	A	CCTTCATACA CATAAA TCCC GCTTGGATGT GCGGCTGCGC ATG-------- ----------		28
94		B	ACTTCATACA CATAAA TCCC GCCTGAACGG TCGTCCGCGC ATG-------- ----------		
95	deaminase	A	.GGCATATAC CATAAT ATGC CGGGCGGTGG CACCATGGCC GTTG------- ----------		29
96		B	CCGCATATAC CATAAT ATGC CGGGCGGGGG CAGGCTGCCC .GTG------- ----------		
97	RNA helic	A	TGTACGAAAC CATAAA ACAA CAGGCCGCGT CAGGGCCGCG CGTG------- ----------		29
98		B	GGGTAGAAAC CATAAA ACAA CAGGCCGCGG CAGGGCG.CG CGTG------- ----------		
99	ORF 06	A	..ACACGCAG TATAAA CGGG GGCCCGGGCG GCGCGTATCA CATG------- ----------		29
100		B	ATACACGTGG TATAAA CAGA GG.CCGGACG GCGCGGACCA CATG------- ----------		
101	tRNA-tyr	A	GCGATAGTTA TTTAAA ACTA GGATGCCGAT CACGGATCGT CCCA------- ----------		29
102		B	GCGATAGTTA TTTAAA ACTA GGATGCCGGG CACCCGTCGT CCCA------- ----------		
103	TBP	A	CCGGGCCCCG GTTAAA ATAG CG.CACGGGC GGATCCTGAC CAATG------ ----------		30
104		B	CCGGGCCCCG GTTAAA ATAG AGTGCGGCCG GGCACCGGAT CAATG------ ----------		
105	TIM	A	GCGTCGATAG AATAAA TACG CGCAGGGGGC CCCGTGGCGC GATCGCCCGT G----------		36
106		B	GCGTCGATAG AATAAA TACG CGC.GGGGCC GCGGTGC... GATCGCCCGT G----------		
107	Hypoth 01	A	ATTTCAACTA CATAAA TGCC TAGTTACGCA GAAATAGCAA ACGACGTACT TCGACTAATG		45
108		B	ACTTCAACTA CATAAA TGCC TAGCTACGCA GAAATATCAA ACAAAGTACT TCGACTAATG		
109	ORF 01	A	ACGGCAGGCT ATTATT ACCT TGCCTTGCGT TGTA //..G CGGGGTGCGG CAGGGGATG		52
110		B	ACGGCAGGCT ATTATT ACCT TGCCGTGTG. TACA //..G AGGGGGCCTG CCGGGAGTG		
111	Methylase	A	CTACAACGAT TTTAAG TCGG CGCCGGGGCA GCCG.//..G ATGTGGGGCA GGCAACATG		104
112		B	CTACAAAGAT TTTAAG ACGG CGCGGGTGCC GCGG.//..T GGCACGGGGG CCTATCTTG		
113	16S RNA	A	TCGGCGATGG TTTATA TGCC CATGGACGGG CCGATCCGAT CGTACGTGAC GC.//..AAT		220
114		B	CCGGCGATGG TTTATA TGCC CATGGACAAG GCGATCCGAT CGTACGTGAC GC.//..AAT		
	Archaeal promoter consensus		YTTAWA		

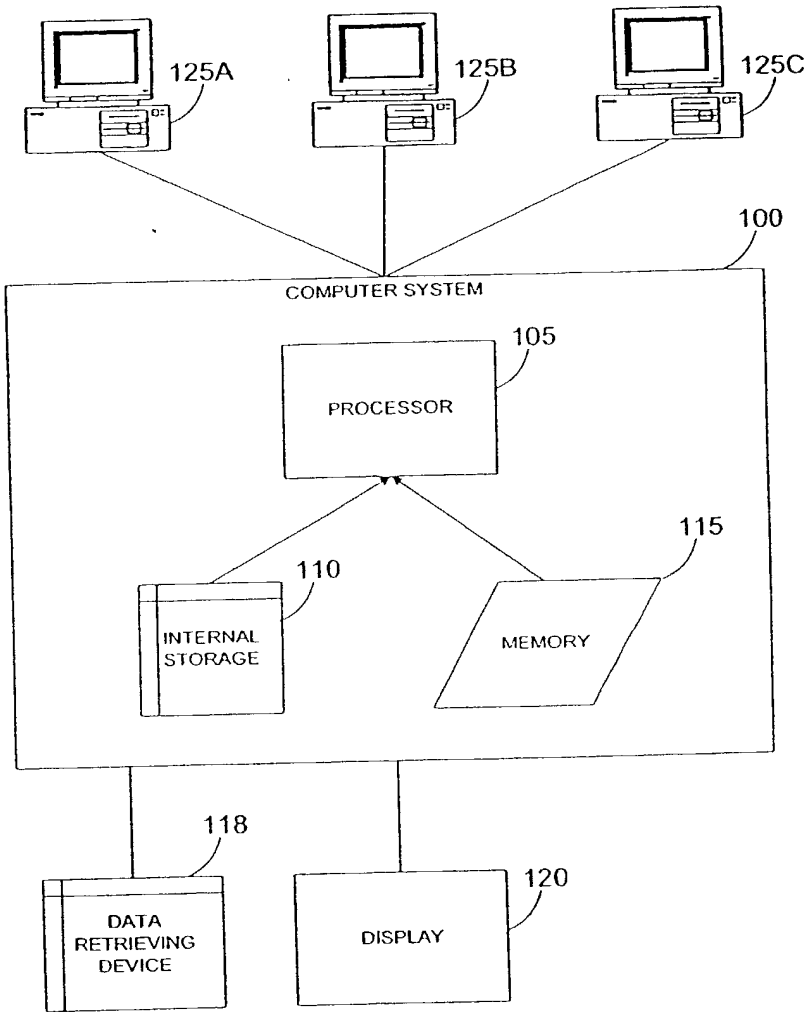

FIGURE 3

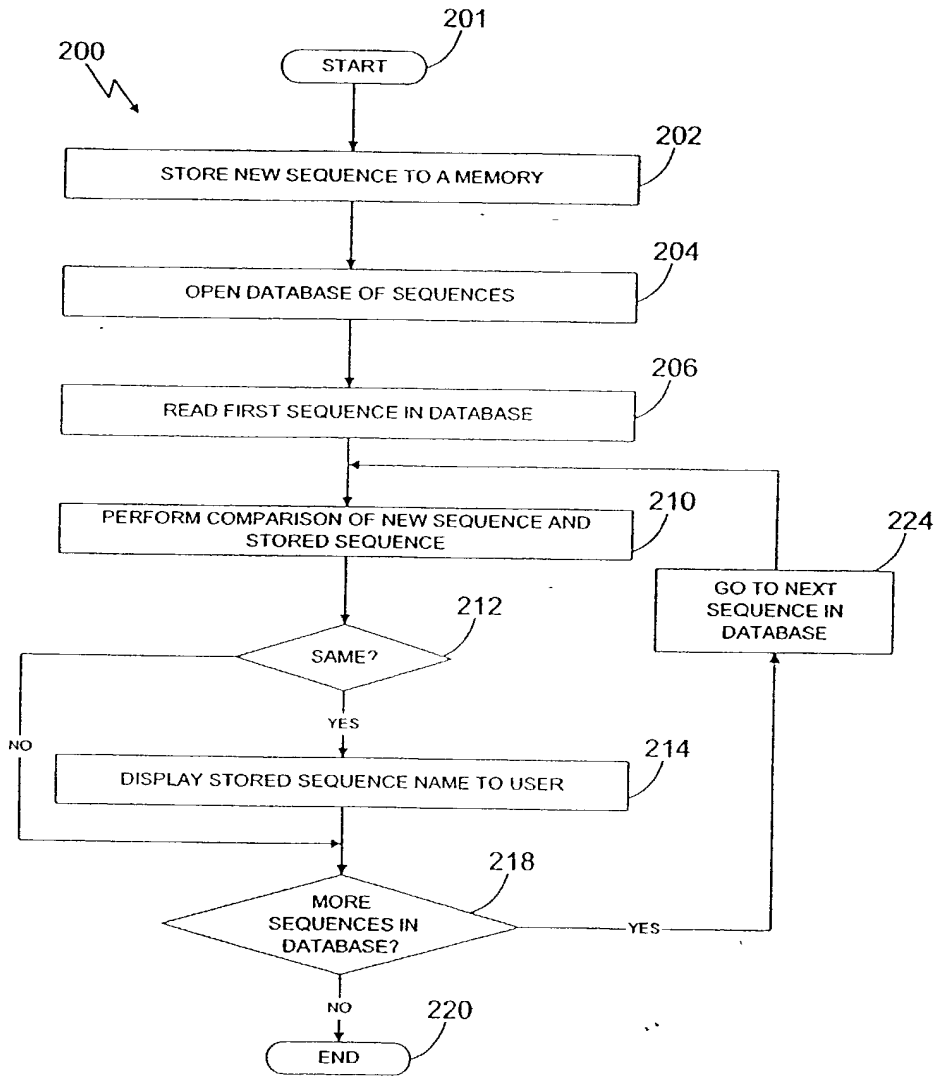
200
201
START
202
STORE NEW SEQUENCE TO A MEMORY
204
OPEN DATABASE OF SEQUENCES
206
READ FIRST SEQUENCE IN DATABASE
210
PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE
212
SAME?
YES
NO
214
DISPLAY STORED SEQUENCE NAME TO USER
218
MORE SEQUENCES IN DATABASE?
YES
NO
220
END
224
GO TO NEXT SEQUENCE IN DATABASE

FIGURE 4

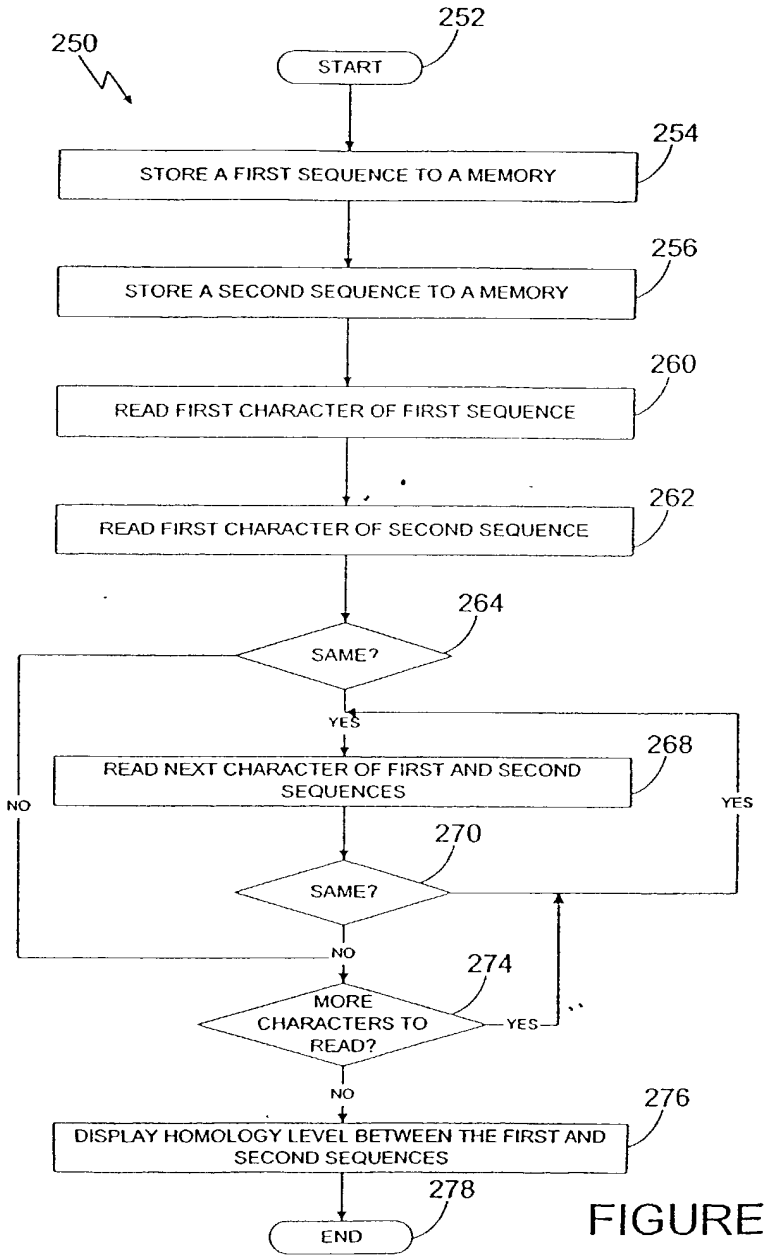

FIGURE 5

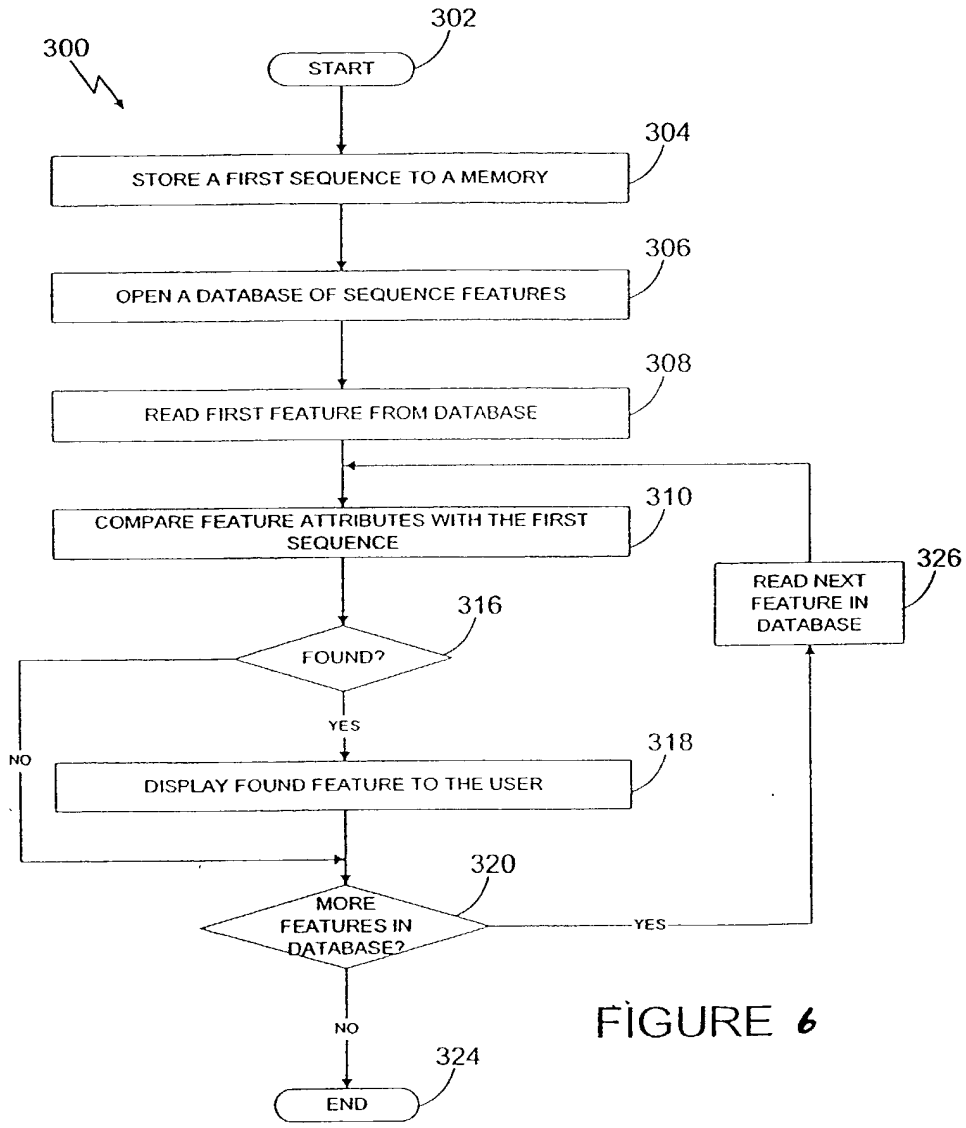
300
302
START
304
STORE A FIRST SEQUENCE TO A MEMORY
306
OPEN A DATABASE OF SEQUENCE FEATURES
308
READ FIRST FEATURE FROM DATABASE
310
COMPARE FEATURE ATTRIBUTES WITH THE FIRST SEQUENCE
316
FOUND?
YES
NO
318
DISPLAY FOUND FEATURE TO THE USER
320
MORE FEATURES IN DATABASE?
YES
NO
324
END
326
READ NEXT FEATURE IN DATABASE

FIGURE 6